

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals S.A.

&lt;120&gt; Novel Compounds

&lt;130&gt; BM45323

&lt;160&gt; 8

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 2310

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 1

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gtagtatccg tatccgcacc gttcagcccc gcaaaacaac aggcggcggc atcagcaaaa	600
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&lt;210&gt; 2

&lt;211&gt; 769

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 2

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Ser	Ser	Leu	Pro	Asn	Lys	Gln	Lys	Ile	Val	Lys	Val	Ser	Phe	Asp	Lys
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Glu	Ile	Val	Asn	Pro	Thr	Gly	Phe	Val	Thr	Ser	Ser	Pro	Ala	Arg	Ile
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Ala	Leu	Asp	Phe	Glu	Gln	Thr	Gly	Ile	Ser	Met	Asp	Gln	Gln	Val	Leu
				65				70						75	
Glu	Tyr	Ala	Asp	Pro	Leu	Leu	Ser	Lys	Ile	Ser	Ala	Ala	Gln	Asn	Ser
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Ser	Arg	Ala	Arg	Leu	Val	Leu	Asn	Leu	Asn	Lys	Pro	Gly	Gln	Tyr	Asn
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Thr	Glu	Val	Arg	Gly	Asn	Lys	Val	Trp	Ile	Phe	Ile	Asn	Glu	Ser	Asp
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Ile Arg Ile Gln Thr Leu Tyr Pro Gly Lys Thr Thr Ala Ala Ala Pro  
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Phe Thr Glu Ser Val Val Ser Val Ser Ala Pro Phe Ser Pro Ala Lys  
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Gln Gln Ala Ala Ala Ser Ala Lys Gln Gln Thr Ala Ala Pro Ala Lys  
195 200 205  
Gln Gln Thr Ala Ala Pro Ala Lys Gln Gln Ala Ala Ala Pro Ala Lys  
210 215 220  
Gln Thr Asn Ile Asp Phe Arg Lys Asp Gly Lys Asn Ala Gly Ile Ile  
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Glu Leu Ala Ala Leu Gly Phe Ala Gly Gln Pro Asp Ile Ser Gln Gln  
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His Asp His Ile Ile Val Thr Leu Lys Asn His Thr Leu Pro Thr Thr  
260 265 270  
Leu Gln Arg Ser Leu Asp Val Ala Asp Phe Lys Thr Pro Val Gln Lys  
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Val Thr Leu Lys Arg Leu Asn Asn Asp Thr Gln Leu Ile Ile Thr Thr  
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Ala Gly Asn Trp Glu Leu Val Asn Lys Ser Ala Ala Pro Gly Tyr Phe  
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340 345 350  
Gln Asp Val Glu Ile Arg Thr Ile Leu Gln Ile Leu Ala Lys Glu Ser  
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Gly Met Asn Ile Val Ala Ser Asp Ser Val Asn Gly Lys Met Thr Leu  
370 375 380  
Ser Leu Lys Asp Val Pro Trp Asp Gln Ala Leu Asp Leu Val Met Gln  
385 390 395 400  
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405 410 415  
Pro Arg Asp Glu Leu Leu Ala Lys Asp Lys Ala Phe Leu Gln Ala Glu  
420 425 430  
Lys Asp Ile Ala Asp Leu Gly Ala Leu Tyr Ser Gln Asn Phe Gln Leu  
435 440 445  
Lys Tyr Lys Asn Val Glu Glu Phe Arg Ser Ile Leu Arg Leu Asp Asn  
450 455 460

Ala Asp Thr Thr Gly Asn Arg Asn Thr Leu Val Ser Gly Arg Gly Ser  
 465 470 475 480  
 Val Leu Ile Asp Pro Ala Thr Asn Thr Leu Ile Val Thr Asp Thr Arg  
 485 490 495  
 Ser Val Ile Glu Lys Phe Arg Lys Leu Ile Asp Glu Leu Asp Val Pro  
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 Ala Gln Gln Val Met Ile Glu Ala Arg Ile Val Glu Ala Ala Asp Gly  
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 580 585 590  
 Ala Leu Asn Leu Glu Leu Ser Ala Ser Glu Ser Leu Ser Lys Thr Lys  
 595 600 605  
 Thr Leu Ala Asn Pro Arg Val Leu Thr Gln Asn Arg Lys Glu Ala Lys  
 610 615 620  
 Ile Glu Ser Gly Tyr Glu Ile Pro Phe Thr Val Thr Ser Ile Ala Asn  
 625 630 635 640  
 Gly Gly Ser Ser Thr Asn Thr Glu Leu Lys Lys Ala Val Leu Gly Leu  
 645 650 655  
 Thr Val Thr Pro Asn Ile Thr Pro Asp Gly Gln Ile Ile Met Thr Val  
 660 665 670  
 Lys Ile Asn Lys Asp Ser Pro Ala Gln Cys Ala Ser Gly Asn Gln Thr  
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 Ile Leu Cys Ile Ser Thr Lys Asn Leu Asn Thr Gln Ala Met Val Glu  
 690 695 700  
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 705 710 715 720  
 Asn Thr Leu Thr Lys Val Pro Leu Leu Gly Asp Ile Pro Val Ile Gly  
 725 730 735  
 Asn Leu Phe Lys Thr Arg Gly Lys Lys Thr Asp Arg Arg Glu Leu Leu  
 740 745 750  
 Ile Phe Ile Thr Pro Arg Ile Met Gly Thr Ala Gly Asn Ser Leu Arg  
 755 760 765  
 Tyr

&lt;210&gt; 3

&lt;211&gt; 2310

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 3

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&lt;210&gt; 4

&lt;211&gt; 769

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 4

Met	Asn	Thr	Lys	Leu	Thr	Lys	Ile	Ile	Ser	Gly	Leu	Phe	Val	Ala	Thr
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Ala	Ala	Phe	Gln	Thr	Ala	Ser	Ala	Gly	Asn	Ile	Thr	Asp	Ile	Lys	Val
							20			25			30		
Ser	Ser	Leu	Pro	Asn	Lys	Gln	Lys	Ile	Val	Lys	Val	Ser	Phe	Asp	Lys
							35			40			45		
Glu	Ile	Val	Asn	Pro	Thr	Gly	Phe	Val	Thr	Ser	Ser	Pro	Ala	Arg	Ile
							50			55			60		
Ala	Leu	Asp	Phe	Glu	Gln	Thr	Gly	Ile	Ser	Met	Asp	Gln	Gln	Val	Leu
	65						70			75			80		
Glu	Tyr	Ala	Asp	Pro	Leu	Leu	Ser	Lys	Ile	Ser	Ala	Ala	Gln	Asn	Ser
							85			90			95		
Ser	Arg	Ala	Arg	Leu	Val	Leu	Asn	Leu	Asn	Lys	Pro	Gly	Gln	Tyr	Asn
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Thr	Glu	Val	Arg	Gly	Asn	Lys	Val	Trp	Ile	Phe	Ile	Asn	Glu	Ser	Asp
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Asp	Thr	Val	Ser	Ala	Pro	Ala	Arg	Pro	Ala	Val	Lys	Ala	Ala	Pro	Ala
							130			135			140		
Ala	Pro	Ala	Lys	Gln	Gln	Ala	Ala	Ala	Pro	Ser	Thr	Lys	Ser	Ala	Val
	145						150			155			160		
Ser	Val	Ser	Lys	Pro	Phe	Thr	Pro	Ala	Lys	Gln	Gln	Ala	Ala	Ala	Pro
							165			170			175		
Phe	Thr	Glu	Ser	Val	Val	Ser	Val	Ser	Ala	Pro	Phe	Ser	Pro	Ala	Lys
							180			185			190		
Gln	Gln	Ala	Ala	Ala	Ser	Ala	Lys	Gln	Gln	Thr	Ala	Ala	Pro	Ala	Lys
							195			200			205		
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							210			215			220		
Gln	Thr	Asn	Ile	Asp	Phe	Arg	Lys	Asp	Gly	Lys	Asn	Ala	Gly	Ile	Ile
	225						230			235			240		

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Leu Gln Arg Ser Leu Asp Val Ala Asp Phe Lys Thr Pro Val Gln Lys  
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Val Leu Ile Asp Pro Ala Thr Asn Thr Leu Ile Val Thr Asp Thr Arg  
485 490 495  
Ser Val Ile Glu Lys Phe Arg Lys Leu Ile Asp Glu Leu Asp Val Pro  
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Ala Gln Gln Val Met Ile Glu Ala Arg Ile Val Glu Ala Ala Asp Gly  
515 520 525  
Phe Ser Arg Asp Leu Gly Val Lys Phe Gly Ala Thr Gly Lys Lys Lys  
530 535 540  
Leu Lys Asn Asp Thr Ser Ala Phe Gly Trp Gly Val Asn Ser Gly Phe  
545 550 555 560  
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Thr Leu Ala Asn Pro Arg Val Leu Thr Gln Asn Arg Lys Glu Ala Lys		
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Ile Glu Ser Gly Tyr Glu Ile Pro Phe Thr Val Thr Ser Ile Ala Asn		
625	630	635
Gly Gly Ser Ser Thr Asn Thr Glu Leu Lys Lys Ala Val Leu Gly Leu		
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Thr Val Thr Pro Asn Ile Thr Pro Asp Gly Gln Ile Ile Met Thr Val		
660	665	670
Lys Ile Asn Lys Asp Ser Pro Ala Gln Cys Ala Ser Gly Asn Gln Thr		
675	680	685
Ile Leu Cys Ile Ser Thr Lys Asn Leu Asn Thr Gln Ala Met Val Glu		
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Asn Gly Gly Thr Leu Ile Val Gly Gly Ile Tyr Glu Glu Asp Asn Gly		
705	710	715
Asn Thr Leu Thr Lys Val Pro Leu Leu Gly Asp Ile Pro Val Ile Gly		
725	730	735
Asn Leu Phe Lys Thr Arg Gly Lys Lys Thr Asp Arg Arg Glu Leu Leu		
740	745	750
Ile Phe Ile Thr Pro Arg Ile Met Gly Thr Ala Gly Asn Ser Leu Arg		
755	760	765
Tyr		

<210> 5  
 <211> 2310  
 <212> DNA  
 <213> Bacteria

<400> 5

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<210> 6  
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<400> 6

Met Asn Thr Lys Leu Thr Lys Ile Ile Ser Gly Leu Phe Val Ala Thr

1

5

10

15

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Ser Ser Leu Pro Asn Lys Gln Lys Ile Val Lys Val Ser Phe Asp Lys  
35 40 45  
Glu Ile Val Asn Pro Thr Gly Phe Val Thr Ser Ser Pro Ala Arg Ile  
50 55 60  
Ala Leu Asp Phe Glu Gln Thr Gly Ile Ser Met Asp Gln Gln Val Leu  
65 70 75 80  
Glu Tyr Ala Asp Pro Leu Leu Ser Lys Ile Ser Ala Ala Gln Asn Ser  
85 90 95  
Ser Arg Ala Arg Leu Val Leu Asn Leu Asn Lys Pro Gly Gln Tyr Asn  
100 105 110  
Thr Glu Val Arg Gly Asn Lys Val Trp Ile Phe Ile Asn Glu Ser Asp  
115 120 125  
Asp Thr Val Ser Ala Pro Ala Arg Pro Ala Val Lys Ala Ala Pro Ala  
130 135 140  
Ala Pro Ala Lys Gln Gln Ala Ala Ala Pro Ser Thr Lys Ser Ala Val  
145 150 155 160  
Ser Val Ser Glu Pro Phe Thr Pro Ala Lys Gln Gln Ala Ala Ala Pro  
165 170 175  
Phe Thr Glu Ser Val Val Ser Val Ser Ala Pro Phe Ser Pro Ala Lys  
180 185 190  
Gln Gln Ala Ala Ala Ser Ala Lys Gln Gln Ala Ala Ala Pro Ala Lys  
195 200 205  
Gln Gln Ala Ala Ala Pro Ala Lys Gln Gln Ala Ala Ala Pro Ala Lys  
210 215 220  
Gln Thr Asn Ile Asp Phe Arg Lys Asp Gly Lys Asn Ala Gly Ile Ile  
225 230 235 240  
Glu Leu Ala Ala Leu Gly Phe Ala Gly Gln Pro Asp Ile Ser Gln Gln  
245 250 255  
His Asp His Ile Ile Val Thr Leu Lys Asn His Thr Leu Pro Thr Thr  
260 265 270  
Leu Gln Arg Ser Leu Asp Val Ala Asp Phe Lys Thr Pro Val Gln Lys  
275 280 285  
Val Thr Leu Lys Arg Leu Asn Asn Asp Thr Gln Leu Ile Ile Thr Thr  
290 295 300  
Ala Gly Asn Trp Glu Leu Val Asn Lys Ser Ala Ala Pro Gly Tyr Phe  
305 310 315 320  
Thr Phe Gln Val Leu Pro Lys Lys Gln Asn Leu Glu Ser Gly Gly Val  
325 330 335  
Asn Asn Ala Pro Lys Thr Phe Thr Gly Arg Lys Ile Ser Leu Asp Phe

340	345	350
Gln Asp Val Glu Ile Arg Thr Ile Leu Gln Ile Leu Ala Lys Glu Ser		
355	360	365
Gly Met Asn Ile Val Ala Ser Asp Ser Val Asn Gly Lys Met Thr Leu		
370	375	380
Ser Leu Lys Asp Val Pro Trp Asp Gln Ala Leu Asp Leu Val Met Gln		
385	390	395
Ala Arg Asn Leu Asp Met Arg Gln Gln Gly Asn Ile Val Asn Ile Ala		
405	410	415
Pro Arg Asp Glu Leu Leu Ala Lys Asp Lys Ala Leu Leu Gln Ala Glu		
420	425	430
Lys Asp Ile Ala Asp Leu Gly Ala Leu Tyr Ser Gln Asn Phe Gln Leu		
435	440	445
Lys Tyr Lys Asn Val Glu Glu Phe Arg Ser Ile Leu Arg Leu Asp Asn		
450	455	460
Ala Asp Thr Thr Gly Asn Arg Asn Thr Leu Ile Ser Gly Arg Gly Ser		
465	470	475
Val Leu Ile Asp Pro Ala Thr Asn Thr Leu Ile Val Thr Asp Thr Arg		
485	490	495
Ser Val Ile Glu Lys Phe Arg Lys Leu Ile Asp Glu Leu Asp Val Pro		
500	505	510
Ala Gln Gln Val Met Ile Glu Ala Arg Ile Val Glu Ala Ala Asp Gly		
515	520	525
Phe Ser Arg Asp Leu Gly Val Lys Phe Gly Ala Thr Gly Lys Lys Lys		
530	535	540
Leu Lys Asn Asp Thr Ser Ala Phe Gly Trp Gly Val Asn Ser Gly Phe		
545	550	555
Gly Gly Asp Asp Lys Trp Gly Ala Glu Thr Lys Ile Asn Leu Pro Ile		
565	570	575
Thr Ala Ala Ala Asn Ser Ile Ser Leu Val Arg Ala Ile Ser Ser Gly		
580	585	590
Ala Leu Asn Leu Glu Leu Ser Ala Ser Glu Ser Leu Ser Lys Thr Lys		
595	600	605
Thr Leu Ala Asn Pro Arg Val Leu Thr Gln Asn Arg Lys Glu Ala Lys		
610	615	620
Ile Glu Ser Gly Tyr Glu Ile Pro Phe Thr Val Thr Ser Ile Ala Asn		
625	630	635
Gly Gly Ser Ser Thr Asn Thr Glu Leu Lys Lys Ala Val Leu Gly Leu		
645	650	655
Thr Val Thr Pro Asn Ile Thr Pro Asp Gly Gln Ile Ile Met Thr Val		
660	665	670

Lys Ile Asn Lys Asp Ser Pro Ala Gln Cys Ala Ser Gly Asn Gln Thr  
675 680 685  
Ile Leu Cys Ile Ser Thr Lys Asn Leu Asn Thr Gln Ala Met Val Glu.  
690 695 700  
Asn Gly Gly Thr Leu Ile Val Gly Gly Ile Tyr Glu Glu Asp Asn Gly  
705 710 715 720  
Asn Thr Leu Thr Lys Val Pro Leu Leu Gly Asp Ile Pro Val Ile Gly  
725 730 735  
Asn Leu Phe Lys Thr Arg Gly Lys Lys Thr Asp Arg Arg Glu Leu Leu  
740 745 750  
Ile Phe Ile Thr Pro Arg Ile Met Gly Thr Ala Gly Asn Ser Leu Arg  
755 760 765  
Tyr

&lt;210&gt; 7

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 7

gggggctagc aataccaaac tgacaaaaat catttcc

37

&lt;210&gt; 8

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 8

gggaaagctt atagcgcagg ctgttgcgg c

31